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SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 49081

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: Al Zhou - Early
Searcher Phone #: 308-4501
Searcher Location: Buried Lab
Date Searcher Picked Up: 8/16/01
Date Completed: 8/17/01
Searcher Prep & Review Time: _____
Clerical Prep Time: 4m
Online Time: 2m

Type of Search

NA Sequence (#) _____
AA Sequence (#) 1
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr. Link _____
Lexis/Nexis _____
Sequence Systems ABSS02
WWW/Internet _____
Other (specify) _____

49081

From: Chan, Christina
Sent: Thursday, August 16, 2001 11:09 AM
To: Huff, Sheela; STIC-Biotech/ChemLib
Subject: RE: RUSh sequence search for 09/428082

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE, 1644
CM 1, Room 9B19
308-3973

CRF6

-----Original Message-----

From: Huff, Sheela
Sent: Thursday, August 16, 2001 9:07 AM
To: Chan, Christina
Subject: RUSh sequence search for 09/428082

Christina--can you please approve this search??

Please search and interference search SEQ ID No. 213 of 09/428082.

Thanks

Sheela Huff
Art Unit 1642
8B07
305-7866

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2001, 14:54:14 ; Search time 10.52 Seconds
(without alignments)
33.929 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSSFWTPYWPYALPL 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 115903 seqs, 16996782 residues

Total number of hits satisfying chosen parameters: 115903

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.5	54.4	22	5	US-09-880-132-58
2	67.5	54.4	22	5	US-09-880-149-58
3	56	45.2	12	5	US-09-880-132-59
4	56	45.2	12	5	US-09-880-149-59
5	50	40.3	549	5	US-09-803-110-9106
6	44	35.5	322	1	PCT-US01-08656-6632
7	44	35.5	336	5	US-09-803-110-8965
8	43	34.7	138	1	PCT-US01-08656-5771
9	43	34.7	194	5	US-09-758-466-6330
10	43	34.7	272	5	US-09-803-110-8377
11	43	34.7	467	5	US-09-664-6108-195
12	42	33.9	127	5	US-09-758-470-402
13	42	33.9	137	5	US-09-758-475-366
14	42	33.9	144	1	PCT-US01-16450-2224
15	42	33.9	168	5	US-09-758-463-977
16	41.5	33.5	495	5	US-09-803-110-11517
17	41	33.1	230	5	US-09-760-455-51
18	41	33.1	270	5	US-09-803-110-12437
19	41	33.1	385	5	US-09-738-626-4559
20	41	33.1	503	5	US-09-738-626-5485
21	41	33.1	684	5	US-09-760-469-1228
22	40.5	32.7	109	5	US-09-694-951B-8
23	40.5	32.7	204	5	US-09-758-445-503
24	40	32.3	58	5	US-09-758-474-784
25	40	32.3	58	5	US-09-758-466-521
26	40	32.3	63	1	PCT-US01-18569-3799
27	40	32.3	159	5	US-09-760-469-1249

28	40	32.3	183	5	US-09-738-626-5595	Sequence 5595, Ap
29	40	32.3	205	5	US-09-602-787A-648	Sequence 648, Ap
30	40	32.3	255	1	PCT-US01-18569-3054	Sequence 3054, Ap
31	40	32.3	273	5	US-09-760-469-1716	Sequence 1716, Ap
32	40	32.3	273	5	US-09-738-626-5643	Sequence 5643, Ap
33	40	32.3	374	5	US-09-738-626-6901	Sequence 6901, Ap
34	40	32.3	425	1	PCT-US01-20592-25	Sequence 25, Appl
35	40	32.3	466	1	PCT-US01-18569-2789	Sequence 2789, Appl
36	40	32.3	466	5	US-09-758-471-4338	Sequence 4338, Ap
37	39.5	31.9	880	1	PCT-US01-20592-36	Sequence 36, Appl
38	39	31.5	99	5	US-09-758-472-5177	Sequence 5177, Ap
39	39	31.5	112	5	US-09-760-479-760	Sequence 760, App
40	39	31.5	133	5	US-09-758-473-1010	Sequence 1010, Ap
41	39	31.5	206	1	PCT-US01-14827-15804	Sequence 15804, A
42	39	31.5	315	5	US-09-602-787A-454	Sequence 454, App
43	39	31.5	330	1	PCT-US01-16450-2183	Sequence 2183, Ap
44	39	31.5	484	5	US-09-602-787A-452	Sequence 452, App
45	39	31.5	521	1	PCT-US01-18569-2799	Sequence 2799, Ap

ALIGNMENTS

RESULT 1
US-09-880-132-58
; Sequence 58, Application US/09880132
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-6
; CURRENT APPLICATION NUMBER: US/09/880,132
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-132-58

Query Match 54.4%; Score 67.5; DB 5; Length 22;
Best Local Similarity 63.2%; Pred. No. 0.00083;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

Qy 6 SPEW---TPYWPYALPL 21
:| | | | | | | | | |
Db 4 TFTWEENAYWPYALPL 22

RESULT 2
US-09-880-149-58
; Sequence 58, Application US/09880149
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-5
; CURRENT APPLICATION NUMBER: US/09/880,149
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 58
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-149-58

Query Match 54.4%; Score 67.5; DB 5; Length 22;
Best Local Similarity 63.2%; Pred. No. 0.00083;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 6 SPEW---TPYYWQPYALPL 21
: | | | | | | | | | |
Db 4 TPTWESNAYWQPYALPL 22

RESULT 3
US-09-880-132-59
; Sequence 59, Application US/09880132
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-6
; CURRENT APPLICATION NUMBER: US/09/880,132
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-132-59

Query Match 45.2%; Score 56; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YWQPYALPL 21
: | | | | | | | | | |
Db 4 YWQPYALPL 12

RESULT 4
US-09-880-149-59
; Sequence 59, Application US/09880149
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-5
; CURRENT APPLICATION NUMBER: US/09/880,149
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-149-59

Query Match 45.2%; Score 56; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YWQPYALPL 21
: | | | | | | | | | |
Db 4 YWQPYALPL 12

RESULT 5
US-09-803-110-9106
; Sequence 9106, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9106
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-9106

Query Match 40.3%; Score 50; DB 5; Length 549;
Best Local Similarity 44.4%; Pred. No. 6.6;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSEFWTPYYWQPYA 18
: | | | | | | | | | |
Db 301 TKPVSLYSLPFWQGVGA 318

RESULT 6
PCT-US01-08656-6632
; Sequence 6632, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 6632
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08656-6632

Query Match 35.5%; Score 44; DB 1; Length 322;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 WTPYYWQPYAL 19

Db 308 WTRYPWQPSSL 318
|| | ||| :|

RESULT 7

US-09-803-110-8965
; Sequence 8965, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 8965
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-8965

Query Match 35.5%; Score 44; DB 5; Length 336;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY 9 WTPYYWQPYALP 19
| | | | |
Db 210 WLGYYNSPTAI 220

RESULT 8

PCT-US01-08656-5771
; Sequence 5771, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5771
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08656-5771

Query Match 34.7%; Score 43; DB 1; Length 138;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 7; Indels 7; Gaps 0;

QY 6 SFENTPYWQPYALP 20
| | | | |
Db 64 SSPMPVTWFPWGLP 78

RESULT 9

US-09-758-466-630
; Sequence 630, Application US/09758466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-466-630

Query Match 34.7%; Score 43; DB 5; Length 194;
Best Local Similarity 44.4%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 NVSFEFTPYWQPYALP 20
| | | | |
Db 138 NEPSNDWDIYYWATEAKP 155

RESULT 10

US-09-803-110-8377
; Sequence 8377, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 8377
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-8377

Query Match 34.7%; Score 43; DB 5; Length 272;
Best Local Similarity 54.5%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 WTPYYWQPYALP 19
| | | | |
Db 146 WVGYYWAPTSL 156

RESULT 11

US-09-664-610B-195
; Sequence 195, Application US/09664610B
; GENERAL INFORMATION:

APPLICANT: CHEN, JIAN
APPLICANT: GODDARD, AUDREY
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: HILLAN, KENNETH
APPLICANT: PENNICA, DIANE
APPLICANT: WOOD, WILLIAM T.
APPLICANT: YUAN, JEAN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: 10466/13
CURRENT APPLICATION NUMBER: US/09/664,610B
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 379
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 195
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
9-664-610B-195

Query Match 34.7%; Score 43; DB 5; Length 467;
Best Local Similarity 45.0%; Pred. No. 56;
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 3 NVSSF--EWTPYWPYALP 20
Db 65 SVPFGEFWFYWQKEIP 84

RESULT 12
US-09-758-470-402
Sequence 402, Application US/09758470
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PN030
CURRENT APPLICATION NUMBER: US/09/758,470
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 722
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-470-402

Query Match 33.9%; Score 42; DB 5; Length 127;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 WTPYWPY 18
Db 25 WRPWWKPR 34

RESULT 13
US-09-758-475-366
Sequence 366, Application US/09758475
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM035
CURRENT APPLICATION NUMBER: US/09/758,475

CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 466
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 366
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (17)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-475-366

Query Match 33.9%; Score 42; DB 5; Length 137;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 TANVSSFETPPYWPYALPL 21
Db 86 TVNVVPFVWTSFFRAQYVP 106

RESULT 14
PCT-US01-16450-2224
Sequence 2224, Application PC/TUS0116450
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA131PCT
CURRENT APPLICATION NUMBER: PCT/US01/16450
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2224
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (131)
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-16450-2224

Query Match 33.9%; Score 42; DB 1; Length 144;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 WTPYWP 14
Db 135 WQPYWP 140

RESULT 15
US-09-758-463-977
Sequence 977, Application US/09758463
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM011
CURRENT APPLICATION NUMBER: US/09/758,463
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065

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; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 977
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-758-463-977

Query Match      33.9%; Score 42; DB 5; Length 168;
Best Local Similarity 46.7%; Pred. NO. 28;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      7 FEWTPYVQPYALPL 21
Db      134 YEWCPSPHPXLLPL 148

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Search completed: August 16, 2001, 14:57:10
Job time: 176 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 12.82 Seconds
(without alignments)
124.779 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSSEFWTPYWPYALPL 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	38.7	525	2 T08027	glucose-1-phosphat
2	47.5	38.3	109	2 H85583	probable tail comp
3	46.5	37.5	201	2 T16878	hypothetical prote
4	46	37.1	856	2 T00349	Avicelase III - As
5	46	37.1	1193	2 JC2489	peptidyl-dipeptida
6	45	36.3	132	2 S03480	T-cell receptor al
7	45	36.3	344	2 T27119	hypothetical prote
8	45	36.3	509	2 T03275	probable cytochrom
9	44	35.5	139	1 RKAUS	ribulose-bisphosph
10	44	35.5	139	1 RKPSL	ribulose-bisphosph
11	44	35.5	161	2 E70530	hypothetical prote
12	44	35.5	254	2 T01109	hypothetical prote
13	44	35.5	301	2 T40593	cytoplasmic dynein
14	44	35.5	314	1 S48466	MOB1 protein [vali
15	44	35.5	334	2 T25055	hypothetical prote
16	44	35.5	401	2 S65138	glutamate dehydrog
17	44	35.5	420	1 JN0854	glutamate dehydrog
18	44	35.5	420	2 A74140	glutamate dehydrog
19	44	35.5	420	2 D75176	glutamate dehydrog
20	44	35.5	422	2 A71038	probable glutamate
21	44	35.5	427	2 S74211	PAS-6/7 protein pr
22	44	35.5	632	2 B69310	mRNA 3'-end proces
23	44	35.5	720	2 T02734	hypothetical prote
24	44	35.5	772	2 E86042	hypothetical prote
25	44	35.5	772	2 B65167	hypothetical 88.1
26	44	35.5	955	2 T39765	probable nuclear m
27	43.5	35.1	283	2 S44848	K06H7.8 protein -
28	43.5	35.1	644	2 H75141	oligopeptide-bindi
29	43	34.7	61	2 S51240	pucA protein - Rh

30 43 34.7 198 2 F70853
31 43 34.7 297 2 A45442
32 43 34.7 342 1 C69395
33 43 34.7 354 2 S75877
34 43 34.7 434 2 S77607
35 43 34.7 437 2 T37469
36 43 34.7 449 2 T19626
37 43 34.7 521 2 C85862
38 43 34.7 529 2 T39841
39 43 34.7 531 1 S54098
40 43 34.7 533 2 T19416
41 43 34.7 624 2 T38006
42 43 34.7 624 2 T20445
43 43 34.7 3036 2 T18995
44 43 34.7 4351 2 T00252
45 42.5 34.3 159 2 S07372

probable leuD prot
transport versicle
H+-transporting At
hypothetical prote
glutamate/glutamin
homogentisate 1,2-
hypothetical prote
hypothetical prote
transcription regu
1-phosphatidylinos
hypothetical prote
probable lysophosp
hypothetical prote
hypothetical prote
MEGFI protein - ra
hypothetical prote

ALIGNMENTS

RESULT 1

T08027

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain - Oriental melon
N:Alternate names: ADP-glucose pyrophosphorylase large chain
C:Species: Cucumis melo var. markuwa Markino (Oriental melon)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T08027

R:Park, S.W.; Kahng, H.Y.; Park, J.O.; Kim, I.J.; Chung, W.I.

submitted to the EMBL Data Library, October 1997

A:Description: Molecular cloning of ADP-glucose pyrophosphorylase small and large sub

A:Reference number: Z16300

A:Accession: T08027

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-525 <PAR>

A:Cross-references: EMBL:AF030383; NID:g2625085; PID:g2625086

A:Experimental source: cv. Euncheon

C:Genetics:

A:Gene: mlf1

C:Function:

A:Description: catalyzes the formation of ADPglucose and pyrophosphate from alpha-D-g

A:Pathway: glycogen/starch biosynthesis (ADPglucose-utilizing)

C:Superfamily: glucose-1-phosphate adenylyltransferase

C:Keywords: nucleotidyltransferase

Query Match 38.7%; Score 48; DB 2; Length 525;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 3 NVSSFSEW---TPYWPYALPL 20

Db 372 NVSRFEFYDPKTPFYTSRPLP 393

RESULT 2

H85583

probable tail component of prophage CP-933K 20976 [imported] - Escherichia coli (stra
C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: H85583

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H85583

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-109 <SFO>

A:Cross-references: GB:AE005174; NID:g12513744; PIDN:AAG55132.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z0976
C:Superfamily: phage lambda minor tail protein M

Query Match 38.3%; Score 47.5; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Oy 4 VSSFEWT-PYVWQP 16

Db 58 VRAFQWTPPYDKP 81

RESULT 3

hypothetical protein T14G12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Sep-2000

C:Accession: T16878

R:Wilcox, L.

Submitted to the EMBL Data Library, November 1995

Description: The sequence of C. elegans cosmid T14G12.

Reference number: Z18596

C:Accession: T16878

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-201 <WIL>

A:Cross-references: EMBL:U41268; NID:g1086843; PID:g1086845; PIDN:AAA82434.1; CESP-T14G12

C:Genetics:

A:Gene: CESP-T14G12.3

A:Introns: 32/2; 61/3; 144/2; 189/1

C:Superfamily: Caenorhabditis elegans hypothetical protein R13H4.2

Query Match

Best Local Similarity 37.5%; Score 46.5; DB 2; Length 201;

Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Oy 2 ANVSFE-WTPYVWQPY 17

Db 65 SNIDRYTFYTPYVWQY 81

RESULT 4

T00349

Avicelase III - Aspergillus aculeatus

C:Species: Aspergillus aculeatus

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Jul-1999

C:Accession: T00349

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-856 <ARA>

A:Cross-references: EMBL:AB015511; NID:d1199887; PID:d1029971

C:Genetics:

A:Gene: avIII

C:Superfamily: fungal cellulose-binding domain homology

F:823-854/Domain: fungal cellulose-binding domain homology <FCB>

Query Match

Best Local Similarity 37.1%; Score 46; DB 2; Length 856;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ANVSFEWTPYVWQ 15

Db 182 SNVTSFTWTGYTFQ 195

RESULT 5

JC2489

peptidyl-dipeptidase A (EC 3.4.15.1) - chicken

N:Alternate names: angiotensin converting enzyme

C:Species: Gallus gallus (chicken)

C>Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999

C:Accession: JC2489

R:Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.

Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994

A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme f

A:Reference number: JC2489; MUID:95110342

A:Accession: JC2489

A:Molecule type: mRNA

A:Residues: 1-1193 <EST>

A:Cross-references: GB:L40175; NID:g685168; PIDN:AAA75554.1; PID:g994708

C:Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc

F:316.331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

Query Match

Best Local Similarity 37.1%; Score 46; DB 2; Length 1193;

Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Oy 1 TANVSFEWTPYVWQPYAL 19

Db 1111 TENGEVLGNPEYSWTPYAV 1129

RESULT 6

S03480

T-cell receptor alpha chain precursor V-J region (TA39) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999

C:Accession: S03480

R:Arden, B.; Klotz, J.L.; Silu, G.; Hood, L.E.

Nature 316, 783-787, 1985

A:Title: Diversity and structure of genes of the alpha family of mouse T-cell antigen

A:Reference number: S03467; MUID:85296324

A:Accession: S03480

A:Molecule type: mRNA

A:Residues: 1-132 <ARD>

A:Cross-references: EMBL:X02929; NID:g54411; PIDN:CAA26684.1; PID:g54412

A>Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-132/Product: T-cell receptor alpha chain (fragment) #status predicted <MAT>

F:1-20/Domain: signal sequence (fragment) #status predicted <SIG>

F:21-112/Domain: V region (TA39) #status predicted <VRE>

F:114-130/Domain: J region #status predicted <JRE>

Query Match

Best Local Similarity 36.3%; Score 45; DB 2; Length 132;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 5 SSFEWTPYVWQ 15

Db 47 STFDYFPYVWQ 57

RESULT 7

T27119

hypothetical protein Y53C10A.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T27119

R:White, S.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z20314

A:Accession: T27119

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <WIL>

A:Cross-references: EMBL:AL033536; PIDN:CAA22140.1; CESP:Y53C10A.6

A:Experimental source: clone Y53C10A

C:Genetics:

A:Gene: CESP:Y53C10A.6

A:Introns: 20/2; 33/1; 61/3; 113/1; 167/3; 233/3; 313/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y53C10A.6

Query Match 36.3%; Score 45; DB 2; Length 344;

Best Local Similarity 47.6%; Pred. No. 46;

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSFETPPYYWQPYALPL 21

||||:|:|:|:|:|:|

123 TANVOAFELPNPKPATRL 143

RESULT 8

T03275

probable cytochrome P450, hypersensitivity-related - common tobacco

N:Alternate names: protein hsr515

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 28-Jul-2000

C:Accession: T03275

R:Czernic, P.; Huang, H.C.; Marco, Y.

Plant Mol. Biol. 31, 255-265, 1996

A:Title: Characterization of hsr201 and hsr515, two tobacco genes preferentially expressed

A:Reference number: Z14876; MUID:96343929

A:Accession: T03275

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-509 <CZE>

A:Cross-references: EMBL:X95342; NID:g1171578; PIDN:CAA64635.1; PID:g1171579

A:Experimental source: cultivar bottom special; tissue-type leaf

C:Genetics:

A:Gene: hsr515

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase

F:302-466/Domain: cytochrome P450 homology <P45>

F:444/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 36.3%; Score 45; DB 2; Length 509;

Best Local Similarity 47.1%; Pred. No. 69;

Matches 8; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 TANVSSFETPPYYWQ 15

||||:|:|:|:|:|

Db 110 TYNYSITWSPYGPYWR 126

RESULT 9

RKAUS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - brown alga (Ectocarpus sil

C:Species: Chloroplast Ectocarpus siliculosus

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999

C:Accession: S13124

R:Valentin, K.; Zetsche, K.

Plant Mol. Biol. 15, 575-584, 1990

A:Title: Rubisco genes indicate a close phylogenetic relation between the plastids of Ch

A:Reference number: S13123; MUID:91338696

A:Accession: S13124

A:Molecule type: DNA

A:Residues: 1-139 <VAL>

A:Cross-references: EMBL:X52503; NID:g11543; PIDN:CAA36744.1; PID:g11545

C:Genetics:

A:Gene: chloroplast

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; c

Query Match 35.5%; Score 44; DB 1; Length 139;

Best Local Similarity 45.5%; Pred. No. 25;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY----YWQPYALPL 21

||||:|:|:|:|:|

Db 34 SVEWTDPPRNSYWELWGLPL 55

RESULT 10

RKPFSL

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - brown alga (Pylaiella l

C:Species: Chloroplast Pylaiella littoralis

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

C:Accession: S17764

R:Assali, N.E.; Martin, W.F.; Sommerville, C.C.; Loiseaux-de Goer, S.

Plant Mol. Biol. 17, 853-863, 1991

A:Title: Evolution of the Rubisco operon from prokaryotes to algae: structure and ana

A:Reference number: S17764; MUID:92003695

A:Accession: S17764

A:Molecule type: DNA

A:Residues: 1-139 <ASS>

A:Cross-references: EMBL:X55372; NID:g14186; PIDN:CAA39052.1; PID:g14188

C:Genetics:

A:Gene: rbcS

A:Superfamily: chloroplast

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase

Query Match 35.5%; Score 44; DB 1; Length 139;

Best Local Similarity 45.5%; Pred. No. 25;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY----YWQPYALPL 21

||||:|:|:|:|:|

Db 34 SVEWTDPPRNSYWELWGLPL 55

RESULT 11

E70530

hypothetical protein Rv2698 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: E70530

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: E70530

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-161 <COL>

A:Cross-references: GB:X96072; GB:AL123456; NID:g3261793; PIDN:CAB09488.1; PID:g21819

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2698

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2698

Query Match 35.5%; Score 44; DB 2; Length 161;

Best Local Similarity 46.2%; Pred. No. 29;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 9 WTPYYWQPYALPL 21

||||:|:|:|:|:|

Db 18 WVPWWWWPLAFAL 30

RESULT 12

T01109
hypothetical protein At2g32980 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T21L14.8
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01109; H84739
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, December 1997
A:Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence.
A:Reference number: Z14209
A:Accession: T01109
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-254 <ROW>
A:Cross-references: EMBL:AC003033; NID:g2702261; PID:g2702269
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Guss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84739
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <STO>
A:Cross-references: GB:AB002093; NID:g2702269; PIDN:AAB91972.1; GSPDB:GN00139
C:Genetics:
A:Gene: T21L14.8; At2g32980
A:Map position: 2
A:Introns: 41/3; 76/3; 99/3; 137/3
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g32980

Query Match 35.5%; Score 44; DB 2; Length 254;
Best Local Similarity 43.8%; Pred. No. 47;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TANVSSEFWTPYVQ 16

||| | | | | |

Db 117 TASVDSFQWSNQFKEP 132

RESULT 13

T40593
cytoplasmic dynein intermediate chain - fission yeast (Schizosaccharomyces pombe) (fragm
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40593
R:Geiger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21938
A:Accession: T40593
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-301 <SE>
A:Cross-references: EMBL:AL035216; PIDN:CAA22821.1; GSPDB:GN00067; SPDB:SPBC646.17c
A:Experimental source: strain 972h-; cosmid c646
C:Genetics:
A:Gene: SPDB:SPBC646.17c
A:Map position: 2

Query Match 35.5%; Score 44; DB 2; Length 301;
Best Local Similarity 57.1%; Pred. No. 56;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ANVSSEFWTPYVQ 15

| | | | | |

Db 176 ALTSSFDWTVRIWQ 189

RESULT 14

S48466
MOBI protein [validated] - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YIL106w
C:Species: Saccharomyces cerevisiae
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: S48466
R:Bowman, S.; Churcher, C.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48455
A:Accession: S48466
A:Molecule type: DNA
A:Residues: 1-314 <ROW>
A:Cross-references: EMBL:Z38125; NID:g558688; PIDN:CAA86274.1; PID:g558700; GSPDB:GNO
Mol. Biol. Cell 9, 29-46, 1998
A:Title: MOBI, an essential yeast gene required for completion of mitosis and mainten
A:Reference number: A59298; MUID:98099687
A:Contents: annotation
C:Genetics:
A:Gene: SGD:MOBI; MIPS:YIL106w
A:Cross-references: SGD:S0001368; MIPS:YIL106w
A:Map position: 9L
A:Introns: 7/2
C:Function:
A:Description: required for normal cell cycle progression; required for completion of
C:Superfamily: Saccharomyces cerevisiae mob1 protein
C:Keywords: phosphoprotein

Query Match 35.5%; Score 44; DB 1; Length 314;
Best Local Similarity 38.9%; Pred. No. 58;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 3 NVSSFEWTPYVQYALP 20

||| | | | | |

Db 98 NVTFNFTSHQRPFLQP 115

RESULT 15

T25055
hypothetical protein T21B4.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T25055
R:Smyle, R.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19974
A:Accession: T25055
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z81124; PIDN:CAB03376.1; GSPDB:GN00020; CESP:T21B4.9
A:Experimental source: clone T21B4
C:Genetics:
A:Gene: CESP:T21B4.9
A:Map position: 2
A:Introns: 120/1; 183/3
C:Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 35.5%; Score 44; DB 2; Length 334;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SFWEFTPYVQPY 17

|| | | | | | |

Db 80 SFFFTPFYVLPY 91

Search completed: August 16, 2001, 14:54:29
Job time: 40 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2001, 07:37:22 ; Search time 10.07 Seconds
 (without alignments)
 72.656 Million cell updates/sec

Title: US-09-428-082-213
 Perfect score: 124
 Sequence: 1 TANVSSEWTPYWPYALPL 21

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Matched: 94743 seqs, 34840360 residues

Total number of hits satisfying chosen parameters: 94743

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	40.3	549	1 BETA_RHIME	P54223 rhizobium m
2	46	37.1	1193	1 ACE_CHICK	Q10751 gallus gall
3	44.5	35.9	664	1 Y4FB_RHISN	P55440 rhizobium s
4	44	35.5	139	1 RBS_ECTSI	P24395 ectocarpus
5	44	35.5	139	1 RBS_PYLII	P23652 pylaialella 1
6	44	35.5	236	1 MOB1_YEAST	P40484 saccharomyc
7	44	35.5	420	1 DHE3_PYRAB	Q47950 pyrococcus
8	44	35.5	420	1 DHE3_PYREN	Q47951 pyrococcus
9	44	35.5	420	1 DHE3_PYRFU	P80319 pyrococcus
10	44	35.5	420	1 DHE3_PYRHO	O52310 pyrococcus
11	44	35.5	427	1 MFGM_BOVIN	O95114 bos taurus
12	44	35.5	772	1 YICI_ECOLI	P31434 escherichia
13	43.5	35.1	283	1 YMX8_CAEEL	P34516 caenorhabdi
14	43	34.7	198	1 LEUD_MYCTU	O53236 mycobacteri
15	43	34.7	297	1 SC13_YEAST	Q04491 saccharomyc
16	43	34.7	342	1 VATC_ARCFU	O29103 archaeoglob
17	43	34.7	434	1 BZTC_RHOCA	O52665 rhodobacter
18	43	34.7	437	1 HGD_CAEEL	O9y041 caenorhabdi
19	43	34.7	478	1 CYCA_GLUSU	Q47945 gluconobact
20	43	34.7	529	1 YBBE_BACSU	P40408 bacillus su
21	42.5	34.3	159	1 Y131_AGRU	P05680 agrobacteri
22	42.5	34.3	275	1 FLA5_PYRKO	O9v247 pyrococcus
23	42.5	34.3	367	1 YMW7_YEAST	Q03151 saccharomyc
24	42	33.9	150	1 YD06_YEAST	P38955 saccharomyc
25	42	33.9	191	1 Y611_METJA	O58028 methanococc
26	42	33.9	535	1 XYNB_BACPU	P07129 bacillus pu
27	42	33.9	562	1 GUN1_ACICE	P54583 acidotherm
28	42	33.9	562	1 YFAA_ECOLI	P17994 escherichia
29	42	33.9	956	1 RRPO_SBMV	P21405 southern be
30	42	33.9	1086	1 CHSD_EMENI	P78611 emericella
31	42	33.9	1184	1 CHSE_EMENI	Q00744 emericella
32	41.5	33.5	230	1 COX2_BRAFL	O47428 branchiosto
33	41.5	33.5	239	1 COX2_BRALA	O79417 branchiosto

RESULT 1

ID	BETA_RHIME	STANDARD	PRT	549 AA
AC	P54223			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	CHOLINE DEHYDROGENASE (EC 1.1.99.1) (CHD).			
GN	BETA.			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Sinorhizobium.			
OX	NCBI_TaxID=382;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=102F34;			
RX	MEDLINE=97286552; PubMed=9141699;			
RA	Pocard J.A., Vincent N., Boncompagni E., Tombras Smith L.,			
RA	Poggi M.-C., Le Rudulier D.;			
RT	"Molecular characterization of the bet genes encoding glycine betaine			
RT	synthesis in Sinorhizobium meliloti 102F34.";			
RL	Microbiology 143:1369-1379(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=102F1;			
RA	Galibert F., Capela D., Hubler-Barloy F., Gatiou M., Batut J.,			
RA	Bolstead P., Gouzy J., Kahn D., Thebault P., Goffeau A.,			
RA	Purnelle B., Pohl T., Bothe G., Schneider S., Portetel D.,			
RA	Vandenbol M., Puehler A., Becker A., Weidner S.;			
RL	Submitted (MAR-2000) to the SWISS-PROT data bank.			
CC	!- FUNCTION: CAN CATALYZE THE OXIDATION OF CHOLINE TO BETAINE			
CC	ALDEHYDE & BETAINE ALDEHYDE TO GLYCINE BETAINE AT THE SAME RATE.			
CC	IT IS INDEPENDENT OF SOLUBLE COFACTORS, AND PROBABLY ELECTRON-			
CC	TRANSFER-LINKED (BY SIMILARITY).			
CC	!- CATALYTIC ACTIVITY: CHOLINE + ACCEPTOR = BETAINE ALDEHYDE +			
CC	REDUCED ACCEPTOR.			
CC	!- COFACTOR: FAD.			
CC	!- PATHWAY: OSMOREGULATORY CHOLINE-GLYCINE BETAINE PATHWAY.			
CC	!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.			
CC	!- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; U39940; AAC13369.1; ..			
DR	InterPro; IPR000172; GMC_Oxred.			
DR	InterPro; IPR000205; NAD_Binding.			
DR	Pfam; PF007732; GMC_Oxred; 1.			
DR	PROSITE; PS00623; GMC_OXRED_1; 1.			
DR	PROSITE; PS00624; GMC_OXRED_2; 1.			
KW	Oxidoreductase; Flavoprotein; FAD; Membrane.			

34	41.5	33.5	500	1	YDAK_YEAST	P28817 saccharomyc
35	41.5	33.5	1756	1	YCF1_PINTH	P41647 pinus thunb
36	41	33.1	102	1	YB41_MYCPN	P75337 mycoplasma
37	41	33.1	136	1	HV01_XENLA	P20956 xenopus lae
38	41	33.1	139	1	RBS_CVLSN	P24683 cylindrothe
39	41	33.1	139	1	RBS_ODOSI	P49521 odontella s
40	41	33.1	139	1	RBS_OILLO	P14961 olisthodisc
41	41	33.1	256	1	HM34_CAEEL	Q94165 caenorhabdi
42	41	33.1	356	1	GLNA_NICPL	P12424 nicotiana p
43	41	33.1	374	1	O71A_DROME	Q9vuk5 drosophila
44	41	33.1	475	1	FAC1_HUMAN	O75844 homo sapien
45	41	33.1	713	1	YHC4_YEAST	P38741 saccharomyc

ALIGNMENTS

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FT NP_BIND 4 33 PAD (ADP PART) (PROBABLE).
FT ACT_SITE 470 470 POTENTIAL.
FT CONFLICT 267 424 A -> R (IN REF. 1).
FT CONFLICT 417 424 RHCVRTR -> DLRAVTR (IN REF. 1).
FT CONFLICT 429 429 Q -> E (IN REF. 1).
SQ SEQUENCE 549 AA; 61291 MW; 29BE064F40CB88F4 CRC64;

Query Match 40.3%; Score 50; DB 1; Length 549;
Best Local Similarity 44.4%; Pred. No. 9.4;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSEFWTPYWPYA 18
| | | | | | | | |
Db 301 TRPVSLSWLPWFQGVA 318

RESULT 2
ID ACE_CHECK STANDARD; PRT; 1193 AA.
AC Q10751;
Q1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DE ANGIOTENSIN-CONVERTING ENZYME (EC 3.4.15.1) (DIPEPTIDYL
GN CARBOXYPEPTIDASE I) (KININASE II) (FRAGMENT).
DN DCPI OR ACE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=95110342; PubMed=7811282;
RA Esther C.R., Thomas K.E., Bernstein K.E.;
RT "Chicken lacks the testis specific isozyme of angiotensin converting
enzyme found in mammals.";
RL Biochem. Biophys. Res. Commun. 205:1916-1921(1994).
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: RELEASE OF A C-TERMINAL DIPEPTIDE,
OLIGOPEPTIDE.-!-XAA-XBB, WHEN XAA IS NOT PRO, AND XBB IS NEITHER
ASP NOR GLU. CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II.
CC -!- COPACITOR: BINDS TWO ZINC IONS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2 (ZINC METALLOPROTEASE).
-----
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-----
EMBL; LA0175; AAA75554.1; -
InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 2.
DR ProDom; PD004184; -; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 2.
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Duplication.
FT NON_TER 1 1
FT DOMAIN <1 1156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1157 1173 POTENTIAL.
FT DOMAIN 1174 1193 CYTOPLASMIC (POTENTIAL).
FT REPEAT 125 481
FT REPEAT 723 1079
FT METAL 288 288 ZINC 1 (CATALYTIC) (BY SIMILARITY).

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FT ACT_SITE 289 289 1 (BY SIMILARITY).
FT METAL 292 292 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 886 886 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 887 887 2 (BY SIMILARITY).
FT METAL 890 890 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 658 658 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1193 AA; 137820 MW; 954472A18EA471C7 CRC64;

Query Match 37.1%; Score 46; DB 1; Length 1193;
Best Local Similarity 42.1%; Pred. No. 66;
Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 TANVSSEFWTPYWPYA 19
| | | | | | | | |
Db 1111 TENGEVLGMWPSWTPYAV 1129

RESULT 3
Y4FB_RHISN STANDARD; PRT; 664 AA.
ID Y4FB_RHISN STANDARD; PRT; 664 AA.
AC P55440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 73.7 KDA PROTEIN Y4FB.
GN Y4FB.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- SIMILARITY: NONE OBVIOUS.
-----
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-----
EMBL; AE000072; AAB91659.1; -
InterPro; IPR001604; Endonuclease.
DR SMART; SM00477; NUC; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 664 AA; 73731 MW; CFCC041FB73C064F CRC64;

Query Match 35.9%; Score 44.5; DB 1; Length 664;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 ANVSSEFWTPYWPYA 14
| | | | | | | | |
Db 506 ANDDTFQWNCSPQYW 521

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RESULT 4
RBS_ECTSI          STANDARD; .      PRT; 139 AA.
AC P24395;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO
DE SMALL SUBUNIT).
GN RBGS.
OS Ectocarpus siliculosus.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales; Ectocarpaceae;
OC Ectocarpus.
OX NCBI_TaxID=2880;
[1]
SEQUENCE FROM N.A.
STRAIN=DILLWIN (LYNGBYE);
RX MEDLINE=91338696; PubMed=2102375;
RA Valentin K., Zetsche K.;
RT "Rubisco genes indicate a close phylogenetic relation between the
RT plastids of Chromophyta and Rhodophyta.";
RL Plant Mol. Biol. 15:575-584(1990).
CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
CC
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CC
CC -----
CC EMBL; X52503; CAA36744.1; -.
CC PIR; S13124; RKAUS.
CC DR HSP; P04716; LRSC.
CC DR Mendel; 4963; ECTsi; rbcS; 1.
CC DR InterPro; IPR000894; RuBisCO_small.
CC DR Pfam; PF00101; RuBisCO_small; 1.
CC DR ProDom; PD000290; -. 1.
CC DR Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;
CC KW Oxidoreductase; Monooxygenase; Chloroplast.
CC SQ SEQUENCE 139 AA; 15938 MW; E316D7803358702D CRC64;

Query Match 35.5%; Score 44; DB 1; Length 139;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YQOPYALPL 21
| | | | |
Db 34 SVEWTDPPHPRNSYWLWGLPL 55

RESULT 5
RBS_PYLII
ID *RBS_PYLII          STANDARD;          PRT; 139 AA.
AC P23652;
DT 01-NOV-1991 (Rel. 20, Created)

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DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO
DE SMALL SUBUNIT).
GN RBGS.
OS Pyraliella littoralis.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pyraliella.
OX NCBI_TaxID=2885;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=91355877; PubMed=2103450;
RA Assali N.E., Mache R., Loiseaux-De Goer S.;
RT "Evidence for a composite phylogenetic origin of the plastid genome
RT of the brown alga Pyraliella littoralis (L.) Kjellm.";
RL Plant Mol. Biol. 15:307-315(1990).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=92003695; PubMed=1840691;
RA Assali N.E., Martin W.F., Sommerville C.C., Loiseaux-De Goer S.;
RT "Evolution of the Rubisco operon from prokaryotes to algae: structure
RT and analysis of the rbcS gene of the brown alga Pyraliella
RT littoralis.";
RL Plant Mol. Biol. 17:853-863(1991).
CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- MISCELLANEOUS: IN THIS ALGA, IN CONTRAST TO PLANTS, THE SMALL
CC SUBUNIT IS ENCODED IN THE CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
CC
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CC
CC -----
CC EMBL; X55372; CAA39052.1; -.
CC PIR; S17764; RKPFSL.
CC DR HSP; P04716; LRSC.
CC DR Mendel; 4021; PYLII; rbcS; 1.
CC DR InterPro; IPR000894; RuBisCO_small.
CC DR Pfam; PF00101; RuBisCO_small; 1.
CC DR ProDom; PD000290; -. 1.
CC DR Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;
CC KW Oxidoreductase; Monooxygenase; Chloroplast.
CC SQ SEQUENCE 139 AA; 15897 MW; 075DC3800915DDC5 CRC64;

Query Match 35.5%; Score 44; DB 1; Length 139;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YQOPYALPL 21
| | | | |
Db 34 SVEWTDPPHPRNSYWLWGLPL 55

RESULT 6
MOBI_YEAST
ID MOBI_YEAST          STANDARD;          PRT; 236 AA.

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AC P40484;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MOBL PROTEIN (MPS1 BINDER 1).
GN MOBL OR YIL106W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR NORMAL CELL PROGRESSION.
CC -!- SIMILARITY: TO YEAST MOB2.
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CC -----
CC EMBL; Z38125; CAA86274.1; ALT_INIT.
CC SGD; S0001368; MOB1.
CC SEQUENCE 236 AA; 27413 MW; B9EA7B368F385D08 CRC64;
DR
SQ
Query Match 35.5%; Score 44; DB 1; Length 236;
Best Local Similarity 38.9%; Pred. NO. 28;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 3 NVSSFEWTPYMQPYALP 20
DB 20 NVTDFNYTFSHOKPELP 37
||:||||:|:|:|
RESULT 7
DHE3_PYRAB STANDARD; PRT; 420 AA.
ID DHE3_PYRAB
AC Q47950;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH OR PAB0391.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 22-255 FROM N.A.
RC STRAIN=GES;
RA Borges K.M., Diruggiero J., Robb F.T.;
RT "Cloning and sequencing of glutamate dehydrogenases from
RT hyperthermophilic archaea.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
CC 2-OXOGLUTARATE + NH(3) + NAD(P)H.
CC -----
AC P40484;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MOBL PROTEIN (MPS1 BINDER 1).
GN MOBL OR YIL106W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR NORMAL CELL PROGRESSION.
CC -!- SIMILARITY: TO YEAST MOB2.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z38125; CAA86274.1; ALT_INIT.
CC SGD; S0001368; MOB1.
CC SEQUENCE 236 AA; 27413 MW; B9EA7B368F385D08 CRC64;
DR
SQ
Query Match 35.5%; Score 44; DB 1; Length 236;
Best Local Similarity 38.9%; Pred. NO. 28;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 3 NVSSFEWTPYMQPYALP 20
DB 20 NVTDFNYTFSHOKPELP 37
||:||||:|:|:|
RESULT 7
DHE3_PYRAB STANDARD; PRT; 420 AA.
ID DHE3_PYRAB
AC Q47950;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH OR PAB0391.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 22-255 FROM N.A.
RC STRAIN=GES;
RA Borges K.M., Diruggiero J., Robb F.T.;
RT "Cloning and sequencing of glutamate dehydrogenases from
RT hyperthermophilic archaea.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
CC 2-OXOGLUTARATE + NH(3) + NAD(P)H.
CC -----
CC -!- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL; AJ248284; CAB49491.1; -.
CC EMBL; LI91116; AAA64796.1; -.
CC HSSP; P80319; IGTW.
CC InterPro; IPR001625; GLFV_dehydrog.
CC Pfam; PF00208; GLFV_dehydrog; 2.
CC PRINTS; PR00082; GLFDHNRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY.
FT NP_BIND 220 226 NAD (POTENTIAL).
FT SEQUENCE 420 AA; 47098 MW; 82F8B343572DFE2B CRC64;
DR
SQ
Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. NO. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 4 VSSFEW----TPYYW 14
DB 351 VSFEWQNTGYW 365
||| ||| | |||
RESULT 8
DHE3_PYREN STANDARD; PRT; 420 AA.
ID DHE3_PYREN
AC Q47951;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA.
OS Pyrococcus endeavori.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=39456;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=ES4;
RX MEDLINE=93352584; PubMed=8349661;
RA Diruggiero J., Robb F.T., Jagus R., Klump H.H., Borges K.M.,
RA Kessel M., Mai X., Adams M.W.W.A.;
RT "Characterization, cloning, and in vitro expression of the extremely
RT thermostable glutamate dehydrogenase from the hyperthermophilic
RT Archaeon, ES4.";
RL J. Biol. Chem. 268:17767-17774(1993).
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
CC 2-OXOGLUTARATE + NH(3) + NAD(P)H.
CC -!- SUBUNIT: HOMOHEXAMER.
CC -!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL; L12408; AAA64795.1; -.
CC InterPro; IPR001625; GLFV_dehydrog.
CC Pfam; PF00208; GLFV_dehydrog; 1.
CC PRINTS; PR00082; GLFDHNRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR
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KW Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY
FT NP_BIND 220 226 NAD (POTENTIAL).
SQ SEQUENCE 420 AA; 47141 MW; 26C571CC5DEF85CB CRC64;

Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 4 VSSFEEW----TPYYW 14
|| ||| |
Db 351 VSYFEWQNTGYW 365

RESULT 9
DHE3_PYRFU STANDARD; PRT; 420 AA.
P80319;
01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010338; PubMed=8406037;
RA Eggen R.I.L., Geerling A.C.M., Waldkoetter K., Antranikian G.,
de Vos V.M.;
RT "The glutamate dehydrogenase-encoding gene of the hyperthermophilic
archaeon Pyrococcus furiosus: sequence, transcription and analysis of
the deduced amino acid sequence.";
RL Gene 132:143-148(1993).
RN [2]
RP SEQUENCE.
RC STRAIN=DSM 3638;
RX MEDLINE=94338538; PubMed=8060497;
RA Maras B., Vallante S., Chiaraluce R., Consalvi V., Politi L.,
de Rosa M., Bossa F., Scandurra R., Barra D.;
RT "The amino acid sequence of glutamate dehydrogenase from Pyrococcus
furiosus, a hyperthermophilic archaeobacterium.";
RL J. Protein Chem. 13:253-259(1994).
RN [3]
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=96164432; PubMed=8591026;
RA Yip K.S.P., Stillman T.J., Britton K.L., Artymiuk P.J., Baker P.J.,
Sedelnikova S.E., Engel P.C., Pasquo A., Chiaraluce R., Consalvi V.,
Scandurra R., Rice D.W.;
RT "The structure of Pyrococcus furiosus glutamate dehydrogenase reveals
a key role for ion-pair networks in maintaining enzyme stability at
extreme temperatures";
RL Structure 3:1147-1158(1995).
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
2-OXOGLOUTARATE + NH(3) + NAD(P)H.
CC -1- SUBUNIT: HOMOHETEROMER.
CC -1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL: M97860; AAA83390.1;
DR PIR: JN0854; JN0854
DR PDB: 1GTM; 11-JAN-97.
DR InterPro: IPR001625; GLFV_dehydrog.
DR Pfam: PF00208; GLFV_dehydrog; 1.

DR PRINTS: PR00082; GLFDHGRGNASE.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase; NAD; NADP; 3D-structure.
FT ACT_SITE 105 105
FT NP_BIND 220 226 NAD (POTENTIAL).
FT CONFLICT 366 366 AW -> WA (IN REF. 2).
FT CONFLICT 366 366 T -> K (IN REF. 2).
SQ SEQUENCE 420 AA; 47114 MW; 673DB20F8764A93C CRC64;

Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 4 VSSFEEW----TPYYW 14
|| ||| |
Db 351 VSYFEWQNTGYW 365

RESULT 10
DHE3_PYRHO STANDARD; PRT; 420 AA.
AC 052310;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH OR PH1593.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL;
RA Gonzalez J.M., Robb F.T., Kato C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
2-OXOGLOUTARATE + NH(3) + NAD(P)H.
CC -1- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL: AF035935; AAB99956.1;
DR EMBL: AP000006; BAA30705.1; ALT_INIT.
DR InterPro: IPR001625; GLFV_dehydrog.
DR Pfam: PF00208; GLFV_dehydrog; 1.
DR PRINTS: PR00082; GLFDHGRGNASE.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY.
FT NP_BIND 220 226 NAD (POTENTIAL).
SQ SEQUENCE 420 AA; 47014 MW; 1198BEC2681B5AA2 CRC64;

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-----
CC EMBL; X91895; CAA62997.1; -.
CC EMBL; S80643; AAB35894.2; -.
DR DR EMBL; Y11719; CAA72406.1; -.
DR HSSP; P00740; IIXA.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000421; FA58_C.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00754; F5_F8_typeC; 2.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00231; FA58C; 2.
DR PROSITE; PS000022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
KW Signal; Glycoprotein; Milk; Repeat; EGF-like domain;
Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 427 LACTADHERIN.
FT DOMAIN 20 59 EGF-LIKE 1.
FT DOMAIN 62 106 EGF-LIKE 2.
FT DOMAIN 109 265 F5/F8 TYPE C 1.
FT DOMAIN 270 427 F5/F8 TYPE C 2.
FT SITE 85 87 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 29 47 BY SIMILARITY.
FT DISULFID 49 58 BY SIMILARITY.
FT DISULFID 66 77 BY SIMILARITY.
FT DISULFID 71 94 BY SIMILARITY.
FT DISULFID 96 105 BY SIMILARITY.
FT DISULFID 109 265 BY SIMILARITY.
FT DISULFID 252 256 O-LINKED (FUC. .) (IN PAS-6).
FT DISULFID 270 427 O-LINKED (FUC. .) (IN PAS-7).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (HYBRID) (IN PAS-6
FT CARBOHYD 34 34 AND PAS-7)).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (HIGH MANNOSE) (IN
PAS-6).
FT VARSPLIC 169 221 MISSING (IN SHORT ISOFORM).
FT CONFLICT 19 19 A -> F (IN REF. 1).
FT CONFLICT 28 28 L -> Q (IN REF. 1).
SQ SEQUENCE 427 AA; 47411 MW; 4CBEE3A1DC4EB24 CRC64;

Query Match 35.5%; Score 44; DB 1; Length 427;
Best Local Similarity 53.8%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TANVSSFETPPYY 13
   | :| :|| |||
DB 294 TWGLSAFSWFPYY 306

RESULT 12
ID YIC1_ECOLI STANDARD; PRT; 772 AA.
AC B31434; P76723;
DT 01-JUL-1993 (Rel. 26, Created)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DD 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHEtical 88.1 KDA PROTEIN IN GLTS-SELC INTERGENIC REGION.
GN YIC1 OR B3656.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
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CC EMBL: L15314; AAA28091.1; -
CC DR PIR: S44848; S44848.
CC DR HSP: Q06486; ICK1.
CC DR WormPep: K06H7.8; CE00259.
CC KW Hypothetical protein.
CC SEQUENCE 283 AA; 32597 MW; 84492C4D99984296 CRC64;
-----
Query Match 35.1%; Score 43.5; DB 1; Length 283;
Best Local Similarity 38.5%; Pred. No. 38;
Matches 5; Conservative 7; Mismatches 0; Indels 1; Gaps 1;
-----
QY 5 SSEFWT-PYVWQP 16
      ::::: |||:|
DB 227 ANYKSDPYHWP 239
-----
RESULT 14
LEUD_MYCTU
ID LEUD_MYCTU STANDARD; PRT; 198 AA.
AC 05236;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
DE (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI).
DE LEUD OR RV2987C OR MVT012.01C.
DE MYcobacterium tuberculosis.
DE Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
DE Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
DE NCBI_TaxID=1773;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Sulston J.E.,
RA Taylor K., Whitehead S., Barrrell B.G.;
RA "Deciphering the Biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
CC -1- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALATE +
CC H(2O) (ALSO CATALYSES 2-ISOPROPYLMALATE + H(2)O = 3-HYDROXY-
CC 4-METHYL-3-CARBOXPENTANONE).
CC -1- PATHWAY: SECOND STEP IN LEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.
-----
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-----
CC EMBL: AL021287; CAA16072.1; -
CC DR TubercuList; RV2987c; -
CC DR InterPro: IPR000573; Aconitase_C.
CC DR Pfam: PF00694; Aconitase_C. 1.
CC KW Leucine biosynthesis; Lvsae.
CC SEQUENCE 198 AA; 21780 MW; 70584A11FB41DB8B CRC64;
-----
Query Match 34.7%; Score 43; DB 1; Length 198;

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DR EMBL: U14913; AAB67426.1; -.
DR PIR: S30803; S30803.
DR PIR: A45442; A45442.
DR PIR: S48559; S48559.
DR SGD: S0004198; SEC13.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRPT.
DR SMART: SM00320; WD40; 6.
DR PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE: PS50082; WD_REPEATS_2; 3.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR KW Transport; Protein transport; Membrane; Endoplasmic reticulum;
DR KW Repeat; WD repeat.
DR REPEAT 7 37
DR FT REPEAT 51 83
DR FT REPEAT 97 131
DR FT REPEAT 143 186
DR FT REPEAT 202 235
DR FT REPEAT 252 282
DR FT MUTAGEN 224 224
DR FT MUTAGEN 262 262
DR FT MUTAGEN 266 266
DR SQ SEQUENCE 297 AA; 33043 MW; A9438884B9CB77FE CRC64;
      S->K: GROWTH INHIBITED ABOVE 30 C.
      W->R: GROWTH INHIBITED ABOVE 30 C.
      G->D: GROWTH INHIBITED ABOVE 34 C.
      A9438884B9CB77FE CRC64;

Query Match 34.7%; Score 43; DB 1; Length 297;
Best Local Similarity 36.8%; Pred. NO. 47;
Matches 7; Conservative 6; Mismatches 6; Indels 0;

QY 1 TANVSFEWTPYKQPYAL 19
   :|:|:|:|:|:|
Db 99 SASVNSVQWAPHEYGPILL 117

Search completed: August 17, 2001, 07:37:41
Job time: 19 sec

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OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 21.95 Seconds
(without alignments)
126.579 Million cell updates/sec

Title: US-09-428-082-213
Perfect score: 124
Sequence: 1 TANVSSFEWTPYWPYALPL 21

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mmc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	44.4	310	2 Q9ZHF8	Q9ZHF8 porphyromon
2	49.5	39.9	509	5 O15712	O15712 paramonium
3	48	38.7	525	10 O22630	O22630 cucumis mel
4	46.5	37.5	201	5 Q22508	Q22508 caenorhabdi
5	46.5	37.5	352	2 Q9FI07	Q9FI07 acinetobact
6	46	37.1	425	10 Q9FYX3	Q9FYX3 lycopersico
7	46	37.1	856	3 O74170	O74170 aspergillus
8	45	36.3	344	5 Q9XW51	Q9XW51 caenorhabdi
9	45	36.3	432	5 Q9NFP2	Q9NFP2 plasmodium
10	45	36.3	509	10 Q43795	Q43795 nicotiana t
11	44.5	35.9	159	5 Q9NME2	Q9NME2 leishmania
12	44	35.5	57	8 Q9TIL8	Q9TIL8 alaria prae
13	44	35.5	57	8 Q9TIL6	Q9TIL6 alaria cras
14	44	35.5	57	8 Q9TIL4	Q9TIL4 alaria nana
15	44	35.5	57	8 Q9TIL2	Q9TIL2 alaria marg
16	44	35.5	57	8 Q9T409	Q9T409 alaria escu
17	44	35.5	57	8 Q9MUK6	Q9MUK6 alaria gran
18	44	35.5	92	14 O55884	O55884 african swi
19	44	35.5	157	2 Q49991	Q49991 mycobacteri

20	44	35.5	161	2	O07200	O07200 mycobacteri
21	44	35.5	254	10	O48767	O48767 arabidopsis
22	44	35.5	281	1	Q9HK70	Q9HK70 thermoplas
23	44	35.5	301	3	O94518	O94518 schizosacch
24	44	35.5	334	5	O18104	O18104 caenorhabdi
25	44	35.5	442	10	Q9LVR2	Q9LVR2 arabidopsis
26	44	35.5	544	3	Q9HG27	Q9HG27 schizosacch
27	44	35.5	544	5	Q9I7F2	Q9I7F2 drosophila
28	44	35.5	596	5	Q9V642	Q9V642 drosophila
29	44	35.5	618	3	O60134	O60134 schizosacch
30	44	35.5	632	1	O29768	O29768 archaeoglob
31	44	35.5	715	5	O61270	O61270 halocynthia
32	44	35.5	720	10	O81072	O81072 arabidopsis
33	44	35.5	947	14	Q9E964	Q9E964 ryegrass mo
34	43.5	35.1	644	1	Q9V057	Q9V057 pyrococcus
35	43	34.7	61	2	Q52654	Q52654 rhodospheo
36	43	34.7	154	6	Q9GMX8	Q9GMX8 macaca fasc
37	43	34.7	166	4	Q9NX18	Q9NX18 homo sapien
38	43	34.7	182	5	Q9WL94	Q9WL94 drosophila
39	43	34.7	240	10	Q9SM56	Q9SM56 psophocarpu
40	43	34.7	354	2	P74242	P74242 synechocyst
41	43	34.7	422	5	Q9VLZ2	Q9VLZ2 drosophila
42	43	34.7	437	5	Q9NJP3	Q9NJP3 caenorhabdi
43	43	34.7	467	4	Q9UJM5	Q9UJM5 homo sapien
44	43	34.7	531	10	Q42582	Q42582 arabidopsis
45	43	34.7	531	10	Q9STZ3	Q9STZ3 arabidopsis

ALIGNMENTS

RESULT 1

Q9ZHF8
ID Q9ZHF8
AC Q9ZHF8
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE HYPOTHETICAL 35.6 KDA PROTEIN.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
OX NCBI_taxid=837;
RN [1]
RP SEQUENCE OF 1-54 FROM N.A.
RC STRAIN=W83;
RX MEDLINE=98013087; PubMed=9353038;
RA Fletcher H.M., Morgan R.M., Macrina F.L.;
RT "Nucleotide sequence of the Porphyromonas gingivalis W83 recA homolog and construction of a recA-deficient mutant.";
RL Infect. Immun. 65:4592-4597(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RA Fletcher H.M., Macrina F.L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RA Fletcher H.M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064682; AAC72889.1;
KW Hypothetical protein.
SQ SEQUENCE 310 AA; 35580 MW; 12979B5284DA56A1 CRC64;

Query Match 44.4%; Score 55; DB 2; Length 310;
Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 8 EWPYWPYPA 18

Db 101 DWLPYWGYS 111

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Best Local Similarity 50.0%; Pred No. 39;
Matches 11; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 3 NVSSFEW----TPYYWQPYALP 20
   ||| ||: ||: ||: ||: ||
Db 372 NVSKFEFYDPKTPPYTSPRFLP 393

RESULT 4
Q22508 PRELIMINARY; PRT; 201 AA.
AC Q22508;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK102C12.3.
GN T14G12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smailson N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RN SEQUENCE FROM N.A.
RA Wilcox L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

```

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RP      SEQUENCE FROM N.A.
RA      Waterston R.;
RL      Submitted (NOV-1995) to the EMBL/GenBank/DBDJ databases.
DR      EMBL: U41268; AAA82434.1; -.
SQ      SEQUENCE      201 AA; 24428 MW; 3802B4733078FC95 CRC64;

Query Match      37.5%; Score 46.5; DB 5; Length 201;
Best Local Similarity 41.2%; Pred. No. 24;
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY      2 ANVSFE-WTPYWPY 17
      :|: : :||:| |
DB      65 SNIDRYTFYFPYWPQY 81

RESULT      5
Q9F1Q7      PRELIMINARY; PRT; 352 AA.
ID      Q9F1Q7      PRELIMINARY;
AC      Q9F1Q7;
DT      01-MAR-2001 (TtEMBLrel. 16, Created)
DT      01-MAR-2001 (TtEMBLrel. 16, Last sequence update)
DT      01-MAR-2001 (TtEMBLrel. 16, Last annotation update)
DE      PUTATIVE TRANSMEMBRANE EFFLUX PROTEIN (FRAGMENT).
OS      Acinetobacter sp. M-1.
OC      Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC      Acinetobacter.
OX      NCBI_TaxID=123502;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=M-1;

```

RESULT	7
ID	074170 PRELIMINARY; PRT; 856 AA.
AC	074170;
DC	AT
DT	01-NOV-1998 (TEMBLrel. 08, Created)
DT	01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT	01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE	AVICELASE III.
GN	AVIII.
OS	Aspergillus aculeatus.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
QC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus;
OX	NCBI_TaxId=5053;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Arai M., Takada G., Kawaguchi T., Sumitani J.;
RT	"Avicelase III from Aspergillus aculeatus.";
RR	

```

Qy      1  TANVSSFETPTYPQVALPL 21
      IIII :II: : : I I
Db      123 TANQAFELPNPKPATRL 143

RESULT      9
Q9NFP2      ID      Q9NFP2      PRELIMINARY;      PRT;      432 AA.
AC      Q9NFP2;
DT      01-OCT-2000 (TReMBLrel. 15, Created)

```


Matches 8; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 TANVSFEWTPY--YQ 15
 | | | | | | | | | |
 Db 110 TYNYSDDITWSPYGPYR 126

RESULT 11
 Q9NME2 PRELIMINARY; PRT; 159 AA.
 ID Q9NME2
 AC Q9NME2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE PROBABLE POSSIBLE DYNEIN HEAVY CHAIN, CYTOSOLIC (FRAGMENT).
 GN LM26.150.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL160493; CAB97768.1; -;
 DR InterPro; IPR001075; -;
 DR ProDom; PD002830; -; 1.
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 17519 MW; 0D5329104AF0DB0E CRC64;

Query Match 35.9%; Score 44.5; DB 5; Length 159;
 Best Local Similarity 44.4%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 ANVSSEFW--TPYIWOP 16
 | | | | | | | | | |
 Db 31 ASVDDFAWYQOLRYIWE 48

RESULT 12
 Q9TIL8 PRELIMINARY; PRT; 57 AA.
 ID Q9TIL8
 AC Q9TIL8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).
 GN R8CS.
 OS Alaria praelonga.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;
 OC Alaria.
 OX NCBI_TaxID=88159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kraan S., Guiry M.D.;
 RT "Sexual hybridization experiments and phylogenetic relationships as
 RT inferred from rubisco spacer sequences in the genus Alaria
 RT (Alariaceae, Phaeophyceae).";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109801; AAF21920.1; -;
 DR InterPro; IPR000894; -;
 DR InterPro; IPR002160; -;
 DR Pfam; PF00101; Rubisco_small.1;
 DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
 Best Local Similarity 45.5%; Pred. No. 15;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YWPYALPL 21
| | | | | : | | : | | |

Db 34 SVEWTDPPHPRNSYWELWGLPL 55

RESULT 13

Q9TIL6 PRELIMINARY; PRT; 57 AA.

AC Q9TIL6; (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)

DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).

GN RBGS.

OS Alaria crassifolia.

OC Chloroplast.

OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;

OC Alaria.

OX NCBI_TaxID=98220;

RN [1]

RP SEQUENCE FROM N.A.

RA Kraan S., Guiry M.D.;

RT "Sexual hybridization experiments and phylogenetic relationships as

inferred from rubisco spacer sequences in the genus Alaria

(Alariaceae, Phaeophyceae)."

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF109802; AAF21922.1; -

DR InterPro; IPR000894; -

DR InterPro; IPR002160; -

DR Pfam; PF00101; RuBisCO_small; 1.

DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

KW Chloroplast.

FT NON_TER 57 57

SQ SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match

Best Local Similarity 35.5%; Score 44; DB 8; Length 57;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YWPYALPL 21
| | | | | : | | : | | |

Db 34 SVEWTDPPHPRNSYWELWGLPL 55

RESULT 14

Q9TIL4 PRELIMINARY; PRT; 57 AA.

AC Q9TIL4; (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)

DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).

GN RBGS.

OS Alaria nana.

OC Chloroplast.

OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;

OC Alaria.

OX NCBI_TaxID=98222;

RN [1]

RP SEQUENCE FROM N.A.

RA Kraan S., Guiry M.D.;

RT "Sexual hybridization experiments and phylogenetic relationships as

inferred from rubisco spacer sequences in the genus Alaria

(Alariaceae, Phaeophyceae)."

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF109803; AAF21924.1; -

DR InterPro; IPR000894; -

DR InterPro; IPR002160; -

DR Pfam; PF00101; RuBisCO_small; 1.

DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

KW Chloroplast. 57 57
SQ SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YWPYALPL 21
| | | | | : | | : | | |

Db 34 SVEWTDPPHPRNSYWELWGLPL 55

RESULT 15

Q9TIL2 PRELIMINARY; PRT; 57 AA.

AC Q9TIL2; (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)

DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).

GN RBGS.

OS Alaria marginata.

OC Chloroplast.

OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;

OC Alaria.

OX NCBI_TaxID=98221;

RN [1]

RP SEQUENCE FROM N.A.

RA Kraan S., Guiry M.D.;

RT "Sexual hybridization experiments and phylogenetic relationships as

inferred from rubisco spacer sequences in the genus Alaria

(Alariaceae, Phaeophyceae)."

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF109804; AAF21926.1; -

DR InterPro; IPR000894; -

DR InterPro; IPR002160; -

DR Pfam; PF00101; RuBisCO_small; 1.

DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

KW Chloroplast. 57 57

FT NON_TER 57 57

SQ SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YWPYALPL 21
| | | | | : | | : | | |

Db 34 SVEWTDPPHPRNSYWELWGLPL 55

Search completed: August 16, 2001, 14:56:53

Job time: 184 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 17.98 Seconds
(without alignments)
70.807 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSFEWYQPYALPL 21

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

11 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0601.*
- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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 - 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
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 - 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	100.0	21	19 AAW68856	Peptide binding in
2	124	100.0	21	19 AAW58089	Interleukin-1 type
3	124	100.0	21	21 AAB17157	IL-1 antagonist pe
4	114	91.9	21	16 AAR90515	Peptide containing
5	114	91.9	21	18 AAW16208	Interleukin-1 type
6	114	91.9	21	18 AAW15973	Interleukin-1 type
7	114	91.9	21	19 AAW68974	Peptide binding in
8	114	91.9	21	19 AAW68611	Peptide binding in
9	114	91.9	21	19 AAW58116	Peptide of the inv
10	114	91.9	21	20 AAY09703	Interleukin-1 type
11	114	91.9	21	21 AAB17757	IL-1 antagonist pe

12	114	91.9	21	21 AAB17794	IL-1 antagonist pe
13	114	91.9	21	21 AAB17814	IL-1 antagonist pe
14	114	91.9	21	21 AAB17899	IL-1 antagonist pe
15	114	91.9	21	21 AAB17913	IL-1 antagonist pe
16	87	70.2	15	16 AAR90521	Interleukin-1 type
17	87	70.2	15	18 AAW15855	Interleukin-1 type
18	87	70.2	15	18 AAW15967	Interleukin-1 type
19	87	70.2	15	19 AAW68931	Peptide binding in
20	87	70.2	15	19 AAW58078	Interleukin-1 type
21	87	70.2	15	20 AAY09695	Interleukin-1 type
22	87	70.2	15	21 AAB17201	IL-1 antagonist pe
23	87	70.2	15	21 AAB17795	IL-1 antagonist pe
24	87	70.2	15	21 AAB17807	IL-1 antagonist pe
25	87	70.2	15	21 AAB17820	IL-1 antagonist pe
26	87	70.2	17	19 AAW68957	Peptide binding in
27	87	70.2	17	19 AAW58118	Peptide of the inv
28	87	70.2	17	20 AAV10070	Interleukin-1 type
29	87	70.2	19	21 AAB17901	IL-1 antagonist pe
30	87	70.2	21	21 AAB17943	IL-1 R antagonist
31	87	70.2	21	21 AAB17944	IL-1 R antagonist
32	87	70.2	248	21 AAB17953	Fc-IL-1 antagonist
33	87	70.2	248	21 AAB17954	IL-1 antagonist-Fc
34	78.5	63.3	21	18 AAW16242	Peptide containing
35	78.5	63.3	21	19 AAW68876	Peptide binding in
36	78.5	63.3	21	19 AAW58358	IL-1RTI binding pe
37	78.5	63.3	21	20 AAY10009	Interleukin-1 type
38	78.5	63.3	21	21 AAB17791	IL-1 antagonist pe
39	78	62.9	15	16 AAR90523	Interleukin-1 type
40	78	62.9	15	16 AAR90522	Interleukin-1 type
41	78	62.9	15	18 AAW15968	Interleukin-1 type
42	78	62.9	15	18 AAW15971	Interleukin-1 type
43	78	62.9	15	19 AAW69003	Peptide binding in
44	78	62.9	15	19 AAW68956	Peptide binding in
45	78	62.9	15	19 AAW58079	Interleukin-1 type

ALIGNMENTS

RESULT 1
AAW68856
ID AAW68856 standard; peptide; 21 AA.
XX
AC AAW68856;
XX
DT 01-OCT-1998 (first entry)
XX
DE Peptide binding interleukin-1 type I receptor.
XX
KW Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1RTI;
KW treatment; IL-1 disorder.
XX
OS Synthetic
XX
PN US5786331-A.
XX
PD 28-JUL-1998.
XX
PF 05-JUN-1995; 95US-0465391.
XX
PR 05-JUN-1995; 95US-0465391.
PR 02-FEB-1994; 94US-0190788.
PR 01-FEB-1995; 95US-0383474.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (HMRI) HOECHST MARION ROUSSEL INC.
XX
PI Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM;
PI Pottorf RS, Yanofsky SD;
XX
DR WPI; 1998-436582/37.
XX
PT Antagonisation of action of interleukin-1 on type I receptor - by

A compound has been developed that binds to an interleukin-1 (IL-1) type I receptor with an IC50 of 2.5 nM or less and has a molecular weight of <3 kD, where the binding of the compound to the receptor is competitively inhibited by a peptide of 8-25 amino acids comprising the core sequence: Z7-28-Q-25-Y-26-Z-29-Z10, where Z5 = pro or azetidine; Z6 = Ser, Ala, Val or Leu; Z7 = Tyr, Trp or Phe; Z8 = Glu, Phe, Val, Trp or Tyr; Z9 = Met, Phe, Val, Arg, Gln, Lys, Thr, Ser, Asp, Leu, Ile or Glu;

CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linker; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antitasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAG69443
 CC to AAG69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 21 AA;

Query Match 100.0%; Score 124; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 QY 1 TANVSSFETPYWQPYALPL 21
 Db 1 tanvssfetpywqpyalpl 21

RESULT 4
 ID AAR90515 standard; peptide; 21 AA.
 XX AAR90515;
 DT 14-MAR-1996 (first entry)
 DE Interleukin-1 type I receptor binding peptide #1.
 KW Interleukin-1 type I receptor; IL-1; IL-1RTI; atherosclerosis;
 KW rheumatoid arthritis; osteoporosis; HIV; AIDS; bacterial infection;
 KW respiratory distress syndrome; acute myelogenous leukaemia;
 KW coal miner pneumococcus; alcoholic cirrhosis; cuprophane haemodialysis;
 KW cardiopulmonary bypass; chronic hepatitis B; thermal injury;
 KW reticulohistiocytosis; sarcoidosis; tuberculosis; obstructive jaundice;
 KW Paget's disease; osteomalacia; IDDM; Kawasaki's disease;
 KW inflammatory bowel disease; sepsis; toxic shock; luteal phase; therapy.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 13..20
 XX /note= "core sequence #1"
 XX
 XX W09520973-A1.
 XX
 XX 10-AUG-1995.
 XX
 XX 01-FEB-1995; 95WO-US01590.
 XX
 XX 02-FEB-1994; 94US-0190788.
 XX
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 XX Baldwin D, Barrett RW, Jacobs JW, Yanofsky SD;
 XX WPI; 1995-283605/37.
 XX
 XX Interleukin-1 type I receptor binding compounds - used e.g. in the
 XX treatment of osteoporosis, HIV and hepatitis B
 XX
 XX Claim 22; Page 53; 56pp; English.
 XX
 XX The sequences represented by R09515-AAR90527 are interleukin-1 type I
 XX receptor (IL-1RTI) binding peptides. These peptides contain the core
 XX sequence represented by AAR83759. These sequences block the binding of

CC IL-1 to IL-1RTI. The sequences were synthesised by using solid phase
 CC synthesis. These sequences are useful in vitro for studying the IL-1
 CC receptor binding process, for developing and assaying other compounds
 CC which bind to the receptor, and for measuring the expression of IL-1RTI
 CC on cell surfaces. They can also be used to monitor the effectiveness of
 CC treatments which influence IL-1 production. They could also be used for
 CC treating disorders which are susceptible to treatment with an IL-1
 CC inhibitor, e.g. atherosclerosis, rheumatoid arthritis, osteoporosis,
 CC HIV, AIDS, bacterial infection, respiratory distress syndrome, acute
 CC myelogenous leukaemia, coal miner pneumococcus, graft vs. host disease,
 CC alcoholic cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass,
 CC chronic hepatitis B, thermal injury, reticulohistiocytosis, sarcoidosis,
 CC tuberculosis, obstructive jaundice, Paget's disease, osteomalacia, IDDM,
 CC Kawasaki's disease, inflammatory bowel disease, sepsis, toxic shock and
 CC luteal phase. These compounds may also be conjugated so that they act
 CC as antagonists, or agonists, of IL-1RTI and may be used to direct a
 CC cytotoxic or therapeutic agent to a cell expressing this receptor.
 XX
 XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 16; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21
 Db 1 tanvssfetpywqpyalpl 21
 RESULT 5
 ID AAW16208 standard; peptide; 21 AA.
 XX AAW16208;
 XX
 XX 19-AUG-1997 (first entry)
 DT Peptide containing QPY or QPY-like motif.
 DE Interleukin-1; type I receptor; IL-1RTI; agonist; antagonist.
 KW
 XX Synthetic.
 XX
 XX W09639165-A1.
 XX
 XX 12-DEC-1996.
 XX
 XX 05-JUN-1996; 96WO-US09835.
 XX
 XX 05-JUN-1995; 95US-0464538.
 XX
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 XX Baldwin D, Barrett RW, Bovy PR, Dharanipragada R;
 XX Jacobs JW, Leahy EM, Pottorf RS, Tomlinson RC, Yanofsky SD;
 XX WPI; 1997-042846/04.
 XX
 XX Interleukin-1 type I receptor inhibitor peptide(s) and compounds -
 XX used to antagonise the activity of IL-1, for treatment of e.g. AIDS,
 XX rheumatoid arthritis, chronic hepatitis B, etc.
 XX
 XX Disclosure; Page 32; 74pp; English.
 XX
 XX The invention relates to peptides which bind to the IL-1 type I
 XX receptor and which comprise the motif WXXG-z1-W or the motif
 XX XQ-25-Y-Z6-XX, in which X can be any one of the 20 genetically
 XX coded L-amino acids or the stereoisomeric D-amino acids or
 XX unnatural amino acids; Z1 is L, I, A or Q; Z5 is P or azetidine
 XX (presumably intended to be azetidine carboxylic acid); and Z6 is S,
 XX A, V or L.
 XX The present sequence is that of a random peptide from a library of

CC peptides containing the "XXQ-25-Y-26-XX" motif, the library being
 CC constructed to screen the peptides for activity.
 CC IL-1 type I receptor-binding peptides may be useful in the treatment
 CC of a variety of IL-1 related disorders including atherosclerosis,
 CC rheumatoid arthritis, osteoporosis, HIV infection and AIDS, bacterial
 CC infection, respiratory distress syndrome, acute myelogenous leukaemia,
 CC graft versus host disease, coal miner pneumoconiosis, alcoholic
 CC cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass, chronic
 CC hepatitis B, tuberculosis, obstructive jaundice, Paget's disease and
 CC osteomalacia, IDDM, Kawasaki's disease, inflammatory bowel disease,
 CC sepsis, toxic shock and luteal phase.
 XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 18; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
 |||||
 Db 1 tanvssfewtpgywqpyalpl 21

RESULT 6
 AAW15973
 ID AAW15973 standard; peptide; 21 AA.
 AC AAW15973;

DT 19-AUG-1997 (first entry)
 DE Interleukin-1 type I receptor binding peptide.
 XX IL-1RtI; agonist; antagonist.

OS Synthetic.
 PN WO9639165-A1.
 XX 12-DEC-1996.
 PD 05-JUN-1996; 95US-099835.
 PF 05-JUN-1995; 95US-0464538.

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

DR Baldwin D, Barrett RW, Bovy PR, Dharanipragada R;
 Jacobs JW, Leahy EM, Pottorf RS, Tomlinson RC, Yanofsky SD;
 WPI; 1997-042846/04.

PT Interleukin-1 type I receptor inhibitor peptide(s) and compounds -
 PT used to antagonise the activity of IL-1, for treatment of e.g. AIDS,
 PT rheumatoid arthritis, chronic hepatitis B, etc.

PS Disclosure; Page 5; 74pp; English.

XX The patent discloses, inter alia, peptides of 8-40 amino acids
 CC in length which bind to the IL-1 type I receptor and which comprise
 CC a core sequence of formula XXQ-25-Y-26-XX, in which X can be any
 CC one of the 20 genetically coded L-amino acids or the stereoisomeric
 CC D-amino acids or unnatural amino acids; 25 is P or azetidine (presumably
 CC intended to be azetidine carboxylic acid); and 26 is S, A, V or L.
 CC These peptides may be used in the treatment of a variety of IL-1
 CC related disorders including atherosclerosis, rheumatoid arthritis,
 CC osteoporosis, HIV infection and AIDS, bacterial infection, respiratory
 CC distress syndrome, acute myelogenous leukaemia, graft versus host
 CC disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
 CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B,
 CC tuberculosis, obstructive jaundice, Paget's disease and osteomalacia,
 CC IDDM, Kawasaki's disease, inflammatory bowel disease, sepsis, toxic

CC shock and luteal phase.
 CC the present sequence is an especially preferred peptide containing
 CC the above motif.
 XX
 SQ Sequence 21 AA;

Query Match 91.9%; Score 114; DB 18; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
 |||||
 Db 1 tanvssfewtpgywqpyalpl 21

RESULT 7
 AAW68974
 ID AAW68974 standard; peptide; 21 AA.
 AC AAW68974;

DT 01-OCT-1998 (first entry)

DE Peptide binding interleukin-1 type I receptor.

XX Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1RtI;
 KW treatment; IL-1 disorder.

XX Synthetic.

XX US5786331-A.

PN 28-JUL-1998.

XX 05-JUN-1995; 95US-0465391.

XX 05-JUN-1995; 95US-0465391.

PR 02-FEB-1994; 94US-0190788.

PR 01-FEB-1995; 95US-0383474.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (HMRI) HOECHST MARION ROUSSEL INC.

XX Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM;
 PI Pottorf RS, Yanofsky SD;

DR WPI; 1998-436582/37.
 XX Antagonisation of action of interleukin-1 on type I receptor - by
 PT contacting receptor with selected peptides

PS Disclosure; Columns 215-216; 118pp; English.

XX AAW68970-82 represent peptide sequences which antagonise the action of
 CC interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1RtI).
 CC The peptides are used in the treatment of disorders mediated by IL-1,
 CC e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
 CC infections, respiratory distress syndrome, acute myelogenous
 CC leukaemia, graft-versus-host disease, pneumoconiosis, cirrhosis,
 CC cuprophane haemodialysis, cardiopulmonary bypass, hepatitis B, thermal
 CC injury, reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive
 CC jaundice, Paget's disease, osteomalacia, diabetes, Kawasaki's disease,
 CC inflammatory bowel disease, sepsis, toxic shock and luteal phase.

SQ Sequence 21 AA;

Query Match 91.9%; Score 114; DB 19; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21

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DE 1 tanvssfewtpgywqpyalpl 21
RESULT 8
ID AAW68611 standard; peptide; 21 AA.
XX AC AAW68611;
XX DT 01-OCT-1998 (first entry)
XX DE Peptide binding interleukin-1 type I receptor.
XX KW Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1r1;
XX KW treatment; IL-1 disorder.
XX OS Synthetic.
XX PA US5786331-A.
XX PD 28-JUL-1998.
XX PF 05-JUN-1995; 95US-0465391.
XX PR 05-JUN-1995; 95US-0465391.
XX PR 02-FEB-1994; 94US-0190788.
XX PR 01-FEB-1995; 95US-0383474.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PA (HMRI) HOECHST MARION ROUSSEL INC.
XX PI Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM;
XX PI Pottorf RS, Yanofsky SD;
XX XX WPI; 1998-436582/37.
XX PT Antagonisation of action of interleukin-1 on type I receptor - by
XX PT contacting receptor with selected peptides
XX PS Disclosure; Column 3; 118pp; English.
XX CC Peptides AAW68611-16 represent peptides that antagonise the action of
XX CC interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1r1).
XX CC The peptides are used in the treatment of disorders mediated by
XX CC IL-1, e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
XX CC infections, respiratory distress syndrome, acute myelogenous leukaemia,
XX CC graft-versus-host disease, pneumoconiosis, cirrhosis, cuprophane
XX CC haemodialysis, cardiopulmonary bypass, hepatitis B, thermal injury,
XX CC reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive jaundice,
XX CC Paget's disease, osteomalacia, diabetes, Kawasaki's disease,
XX CC inflammatory bowel disease, sepsis, toxic shock and luteal phase.
XX XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 19; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPTYYWQPYALPL 21
Db 1 tanvssfewtpgywqpyalpl 21

RESULT 9
ID AAW58116 standard; peptide; 21 AA.
XX AC AAW58116;
XX AC AAW58116;
XX DT 14-AUG-1998 (first entry)
XX DE Interleukin-1 type I receptor binding peptide #20.

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DE Peptide of the invention SEQ ID NO:17 from US 5767234 Example 2.
XX Interleukin-1 type I receptor; binding peptide; IL-1r; IL-1r1;
XX KW competitive inhibition; cytokine; blocker; IL-1 related disorder;
XX KW diagnosis; atherosclerosis; rheumatoid arthritis; osteoporosis.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX US5767234-A.
XX PD 16-JUN-1998.
XX PF 01-FEB-1995; 95US-0383474.
XX PR 01-FEB-1995; 95US-0383474.
XX PR 02-FEB-1994; 94US-0190788.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX XX Baldwin D, Barrett RW, Jacobs JW, Yanofsky SD;
XX PI WPI; 1998-361782/31.
XX DR Peptide(s) that bind to interleukin-1 type I receptor - useful in
XX PT screening assays for interleukin receptors blockers, diagnosis and
XX PT therapy
XX XX Example 2; Column 28; 89pp; English.
XX CC A compound has been developed that binds to an interleukin-1 (IL-1)
XX CC type I receptor with an IC50 of 2.5 mM or less and has a molecular
XX CC weight of <3 kD, where the binding of the compound to the receptor is
XX CC competitively inhibited by a peptide of 8-25 amino acids comprising the
XX CC core sequence: 27-28-Q-25-Y-26-Z9-Z10, where 25 = pro or azetidine; 26 =
XX CC Ser, Ala, Val or Leu; 27 = Tyr, Trp or Phe; 28 = Glu, Phe, Val, Trp or
XX CC Tyr; 29 = Met, Phe, Val, Arg, Gln, Lys, Thr, Ser, Asp, Leu, Ile or Glu;
XX CC and Z10 = Glu, Leu, Trp, Val, His, Ile, Gly, Ala, Asp, Tyr, Asn, Gln or
XX CC pro. Peptides of the invention are used in screening assays for IL-1
XX CC receptor blockers. They are also used as probes for detecting IL-1 type I
XX CC receptor expression on the surface of cells. The peptides are useful in
XX CC treating IL-1-related disorders, e.g. atherosclerosis, rheumatoid
XX CC arthritis, osteoporosis, HIV infection, AIDS, bacterial infection,
XX CC respiratory distress syndrome, acute myelogenous leukaemia (AML), graft
XX CC versus host disease, coal miner pneumoconiosis, alcoholic cirrhosis,
XX CC cuprophane haemodialysis, cardiopulmonary bypass, chronic hepatitis B,
XX CC thermal injury, reticulohistiocytosis, sarcoidosis, tuberculosis,
XX CC obstructive jaundice, Paget's disease and osteomalacia, Kawasaki's
XX CC disease, inflammatory bowel disease, sepsis, toxic shock, and luteal
XX CC phase. The present sequence represents a peptide from the present
XX CC invention.
XX XX Sequence 21 AA;

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Query Match 91.9%; Score 114; DB 19; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPTYYWQPYALPL 21
Db 1 tanvssfewtpgywqpyalpl 21

RESULT 10
ID AAY09703 standard; peptide; 21 AA.
XX AC AAY09703;
XX AC AAY09703;
XX DT 07-MAY-1999 (first entry)
XX DE Interleukin-1 type I receptor binding peptide #20.

```


XX Interleukin-1 type I receptor; IL-1RtI; inflammatory bowel disease;
 KW rheumatoid arthritis; osteoarthritis; psoriasis; encephalitis;
 KW glomerulonephritis; respiratory distress syndrome.
 XX Synthetic.
 OS
 PN US5880096-A.
 XX
 XX 09-MAR-1999.
 PD
 XX
 XX 05-JUN-1995; 35US-0463076.
 PF
 XX
 XX 05-JUN-1995; 35US-0463076.
 PR
 XX 02-FEB-1994; 94US-0190788.
 PR
 XX 01-FEB-1995; 95US-0383474.
 XX
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PA
 XX
 XX Barrett RW, Yanofsky SD;
 PI
 WPI; 1999-204004/17.
 PS
 XX New peptides which bind to the interleukin-1 type I receptor
 PT (IL-1RtI) - useful for the study of IL-1RtI mediated activities and
 PT the treatment/prevention of diseases with an inappropriate
 PT production or response to interleukin-1
 XX
 XX Disclosure; Column 3; 120pp; English.
 XX
 CC The invention relates to new peptides which bind to the
 CC interleukin-1 type I receptor (IL-1RtI). These include 'lead'
 CC peptides identified using random peptide diversity generating
 CC systems (e.g. 'peptides on phage' and 'peptides on plasmids'
 CC systems) and derivatives of the 'lead' peptides which have a
 CC similar structure or shape as the lead compounds but which differ
 CC with respect to susceptibility to hydrolysis or proteolysis and/or
 CC with respect to biological properties.
 CC These peptides are useful as agonists/antagonists for the study of
 CC IL-1RtI mediated activities (e.g. as labels and probes), for the
 CC identification of new IL-1 receptor blockers, and for the
 CC identification, diagnosis and treatment/prevention of diseases with
 CC an inappropriate production or response to IL-1, e.g. rheumatoid
 CC arthritis, osteoarthritis, psoriasis, inflammatory bowel disease,
 CC encephalitis, glomerulonephritis, and respiratory distress syndrome.
 XX
 XX Sequence 21 AA;
 SQ

Query Match 91.9%; Score 114; DB 20; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TANVSSFEWTPYWPYALPL 21
 Db 1 tanvssfewtpgywqypalpl 21
 ||||||||| |||||||||
 RESULT 11
 AAB17757
 ID AAB17757 standard; Peptide; 21 AA.
 XX
 XX AAB17757;
 AC
 XX
 XX 31-OCT-2000 (first entry)
 DT
 XX
 XX IL-1 antagonist peptide sequence SEQ ID NO: 861.
 DE
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CFLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;

KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX Synthetic.
 OS
 PN WO200024782-A2.
 XX
 XX 04-MAY-2000.
 PD
 XX
 XX 25-OCT-1999; 99WO-US25044.
 PF
 XX
 XX 23-OCT-1998; 98US-0105371.
 PR
 XX 22-OCT-1999; 99US-0428082.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI
 XX WPI; 2000-350702/30.
 DR
 XX
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases.
 PT
 XX
 XX Claim 10; Page 490; 608pp; English.
 PS
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 21 AA;
 SQ

Query Match 91.9%; Score 114; DB 21; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TANVSSFEWTPYWPYALPL 21
 Db 1 tanvssfewtpgywqypalpl 21
 ||||||||| |||||||||
 RESULT 12
 AAB17794
 ID AAB17794 standard; Peptide; 21 AA.
 XX
 XX AAB17794;
 AC
 XX
 XX 31-OCT-2000 (first entry)
 DT
 XX
 XX IL-1 antagonist peptide sequence SEQ ID NO: 898.
 DE
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CFLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;

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XX OS Synthetic.
XX PN WO200024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US25044.
XX PR 23-OCT-1998; 98US-0105371.
XX PR 22-OCT-1999; 99US-0428082.
XX PA (AMGE-) AMGEN INC.
XX PI Feige U, Liu C, Cheetham J, Boone TC;
XX DR WPT: 2000-350702/30.
XX PT Novel composition of matter comprising an Fc domain and
XX PT pharmacologically active peptides, useful for treating cancer and
XX PT autoimmune diseases.
XX PS Claim 10; Page 514; 608pp; English.
XX CC The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
XX CC where P1, P2, P3, and P4 = are each independently sequences of
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
XX CC independently linkers; and a, b, c, d, e, and f = are each independently
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
XX CC activities. DNAs, vectors and host cells from the present invention can
XX CC be used for producing pharmaceutical compositions. The compositions are
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer
XX CC half-life or incorporate functions such as Fc receptor binding, protein
XX CC A binding, complement fixation, and possibly placental transfer. AAA69443
XX CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
XX CC sequences used in the exemplification of the present invention.
XX SQ Sequence 21 AA;

Query Match 91.9%; Score 114; DB 21; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETWPPYWPVALPL 21
Db 1 tanvssfetwppgywqpyalpl 21
|||||
|||||

RESULT 14
AAB17899
ID AAB17899 standard; Peptide; 21 AA.
XX AAB17899;
XX AC
XX XX
XX DT 31-OCT-2000 (first entry)
XX DE
XX DE IL-1 antagonist peptide sequence SEQ ID NO:1003.
XX XX
XX XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
XX KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
XX KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX KW vascular endothelial growth factor; matrix metalloproteinase;
XX KW asthma; thrombosis; pharmaceutical.
XX XX

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OS	Synthetic.
XX	
PN	WO200024782-A2.
XX	
PD	04-MAY-2000.
XX	
XX	
PF	25-OCT-1999; 99WO-US25044.
XX	
XX	23-OCT-1998; 98US-0105371.
PR	22-OCT-1999; 99US-0428082.
XX	
XX	(AMGE-) AMGEN INC.
PA	
XX	
PI	Feige U, Liu C, Cheetham J, Boone TC;
XX	
PI	WPI; 2000-350702/30.
XX	
XX	
PT	Novel composition of matter comprising an Fc domain and
PT	pharmacologically active peptides, useful for treating cancer and
PT	autoimmune diseases.
XX	
XX	Claim 10; Page 547; 608pp; English.
XX	
CC	The present invention describes composition of matter (I) comprising an
CC	Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC	(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC	independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC	-(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC	where P1, P2, P3, and P4 = are each independently sequences of
CC	pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC	independently linkers; and a, b, c, d, e, and f = are each independently
CC	0 or 1, provided that at least 1 of a and b is 1. The composition can
CC	have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC	activities. DNAs, vectors and host cells from the present invention can
CC	be used for producing pharmaceutical compositions. The compositions are
CC	useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC	The use of an Fc domain (rather than a Fab domain) can provide a longer
CC	half-life or incorporate functions such as Fc receptor binding, protein
CC	A binding, complement fixation, and possibly placental transfer. AAA69443
CC	to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC	sequences used in the exemplification of the present invention.
XX	
SQ	Sequence 21 AA;
XX	
Query Match	91.9%; Score 114; DB 21; Length 21;
Best Local Similarity	95.2%; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
DB	1 TANVSSFEWTPYTWQPYALPL 21
	1 tanvssfeWtpgywqpyalpl 21
RESULT 15	
AAB17913	
ID	AAB17913 standard; Peptide; 21 AA.
XX	
AC	AAB17913;
XX	
DT	31-OCT-2000 (first entry)
XX	
DE	IL-1 antagonist peptide sequence SEQ ID NO:1017.
XX	
KW	Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW	autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW	immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW	MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW	cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW	vascular endothelial growth factor; matrix metalloproteinase;
KW	asthma; thrombosis; pharmaceutical.
XX	
OS	Synthetic.

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XX PN WO2000024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US25044.
XX PR 23-OCT-1998; 98US-0105371.
XX PR 22-OCT-1999; 99US-0428082.
XX PA (AMGE-) AMGEN INC.
XX PF Feige U, Liu C, Cheetham J, Boone TC;
XX DR WPI; 2000-350702/30.
XX PT Novel composition of matter comprising an Fc domain and
XX PT pharmacologically active peptides, useful for treating cancer and
XX PT autoimmune diseases -
XX PS Claim 10; Page 553; 608pp; English.
XX CC The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
XX CC where P1, P2, P3, and P4 = are each independently sequences of
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
XX CC independently linkers; and a, b, c, d, e, and f = are each independently
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
XX CC activities. DNAs, vectors and host cells from the present invention can
XX CC be used for producing pharmaceutical compositions. The compositions are
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer
XX CC half-life or incorporate functions such as Fc receptor binding, protein
XX CC A binding, complement fixation, and possibly placental transfer. AAA69443
XX CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
XX CC sequences used in the exemplification of the present invention.
XX SQ Sequence 21 AA;

Query Match 91.9%; Score 114; DB 21; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 TANVSSSFEWTPYMQPYALPL 21
Db 1 tanvsssfewtpgywqpyalpl 21

Search completed: August 16, 2001, 14:54:53
Job time: 64 sec

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Search completed: August 16, 2001, 14:54:53
Job time: 64 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 12.18 seconds
(without alignments)
35.501 Million cell updates/sec

Title: US-09-428-082-213
Perfect score: 124
Sequence: 1 TANVSSFEWTPYQPYALPL 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	100.0	21	1 US-08-190-788A-11	Sequence 11, Appl
2	124	100.0	21	1 US-08-190-788A-256	Sequence 256, App
3	124	100.0	21	1 US-08-465-391A-256	Sequence 256, App
4	124	100.0	21	2 US-08-464-538B-256	Sequence 256, App
5	114	91.9	21	1 US-08-383-474B-17	Sequence 17, Appl
6	114	91.9	21	1 US-08-465-391A-11	Sequence 11, Appl
7	114	91.9	21	1 US-08-465-391A-374	Sequence 374, App
8	114	91.9	21	2 US-08-464-538B-11	Sequence 11, Appl
9	114	91.9	21	2 US-08-464-538B-371	Sequence 371, App
10	114	91.9	21	2 US-08-463-076E-20	Sequence 20, Appl
11	87	70.2	15	1 US-08-383-474B-10	Sequence 10, Appl
12	87	70.2	15	1 US-08-465-391A-331	Sequence 331, App
13	87	70.2	15	2 US-08-464-538B-329	Sequence 329, App
14	87	70.2	15	2 US-08-463-076E-12	Sequence 12, Appl
15	87	70.2	17	1 US-08-383-474B-300	Sequence 300, Appl
16	87	70.2	17	1 US-08-465-391A-357	Sequence 357, App
17	87	70.2	17	2 US-08-464-538B-354	Sequence 354, App
18	87	70.2	17	2 US-08-463-076E-391	Sequence 391, App
19	78.5	63.3	21	1 US-08-190-788A-276	Sequence 276, App
20	78.5	63.3	21	1 US-08-383-474B-279	Sequence 279, App
21	78.5	63.3	21	1 US-08-465-391A-276	Sequence 276, App
22	78.5	63.3	21	2 US-08-464-538B-276	Sequence 276, App
23	78.5	63.3	21	2 US-08-463-076E-330	Sequence 330, App
24	78	62.9	15	1 US-08-383-474B-11	Sequence 11, Appl
25	78	62.9	15	1 US-08-383-474B-14	Sequence 14, Appl
26	78	62.9	15	1 US-08-465-391A-356	Sequence 356, App
27	78	62.9	15	1 US-08-465-391A-403	Sequence 403, App

28	78	62.9	15	2 US-08-464-538B-353	Sequence 353, App
29	78	62.9	15	2 US-08-464-538B-400	Sequence 400, App
30	78	62.9	15	2 US-08-463-076E-13	Sequence 13, Appl
31	78	62.9	15	2 US-08-463-076E-16	Sequence 16, Appl
32	76	61.3	21	1 US-08-190-788A-248	Sequence 248, App
33	76	61.3	21	1 US-08-383-474B-251	Sequence 251, App
34	76	61.3	21	1 US-08-465-391A-248	Sequence 248, App
35	76	61.3	21	2 US-08-464-538B-248	Sequence 248, App
36	76	61.3	21	2 US-08-463-076E-305	Sequence 305, App
37	75	60.5	21	1 US-08-190-788A-246	Sequence 246, App
38	75	60.5	21	1 US-08-383-474B-249	Sequence 249, App
39	75	60.5	21	1 US-08-465-391A-246	Sequence 246, App
40	75	60.5	21	2 US-08-464-538B-246	Sequence 246, App
41	75	60.5	21	2 US-08-463-076E-303	Sequence 303, App
42	73	58.9	15	1 US-08-383-474B-12	Sequence 12, Appl
43	73	58.9	15	1 US-08-465-391A-402	Sequence 402, App
44	73	58.9	15	2 US-08-464-538B-399	Sequence 399, App
45	73	58.9	15	2 US-08-463-076E-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-190-788A-11
; Sequence 11, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190.788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-190-788A-11

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 2

US-08-190-788A-256
; Sequence 256, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190.788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-190-788A-256

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 3

US-08-465-391A-256
; Sequence 256, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.

; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorff, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331v1el, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-465-391A-256

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 4

US-08-464-538B-256
; Sequence 256, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorff, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 256:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-256

Query Match 100.0%; Score 124; DB 2; Length 21;
Best Local Similarity 100.0%; Pred No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TANVSSFEWTPYYQPYALPL 21
Db 1 TANVSSFEWTPYYQPYALPL 21

RESULT 5
US-08-383-474B-17
Sequence 17, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-17

Query Match 91.98; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 TANVSSFEWTPYYQPYALPL 21
Db 1 TANVSSFEWTPYYQPYALPL 21

RESULT 6
US-08-465-391A-11
Sequence 11, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: No. 5786331v1el, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-11

Query Match 91.9%; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TANVSSFEWTPYQWYALPL 21
|||||||
1 TANVSSFEWTPYQWYALPL 21

RESULT 7

US-08-465-391A-374
Sequence 374, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331v1el, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:

NAME: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-374

Query Match 91.9%; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYQWYALPL 21
|||||||
DB 1 TANVSSFEWTPYQWYALPL 21

RESULT 8

US-08-464-538B-11
Sequence 11, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-11

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 9

US-08-464-538B-371
; Sequence 371, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-371

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 10

US-08-463-076E-20
; Sequence 20, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.

REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-0018500S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-20

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 11

US-08-383-474B-10
; Sequence 10, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/383,474B
;; FILING DATE: 01-FEB-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/190,788
;; FILING DATE: 02-FEB-1994
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens, Lauren L.
;; REGISTRATION NUMBER: 36,691
;; REFERENCE/DOCKET NUMBER: 1019.3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-496-2300
;; TELEFAX: 415-424-0832
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-383-474B-10

Query Match 70.2%; Score 87; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQPYALPL 21
||||| |||||
DB 1 FEWTPYQPYALPL 15

RESULT 12
US-08-465-391A-331
; Sequence 331, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/190,788
;; FILING DATE: 02-FEB-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5786331v1el, Vern
;; REGISTRATION NUMBER: 32,483
;; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 331:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-465-391A-331

Query Match 70.2%; Score 87; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQPYALPL 21
||||| |||||
DB 1 FEWTPYQPYALPL 15

RESULT 13
US-08-464-538B-329
; Sequence 329, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-329

Query Match 70.2%; Score 87; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
1 FEWTPGYWQYALPL 15

RESULT 14
US-08-463-076E-12
Sequence 12, Application US/08463076E
Patent No. 5880096
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-12

Query Match 70.2%; Score 87; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
Db 1 FEWTPGYWQYALPL 15

RESULT 15
US-08-383-474B-300
Sequence 300, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 17
OTHER INFORMATION: /note= "C-terminal Asp is amidated."
US-08-383-474B-300

Query Match 70.2%; Score 87; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.9e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
Db 1 FEWTPGYWQYALPL 15

Search completed: August 16, 2001, 14:54:09
Job time: 20 sec

